

1/17

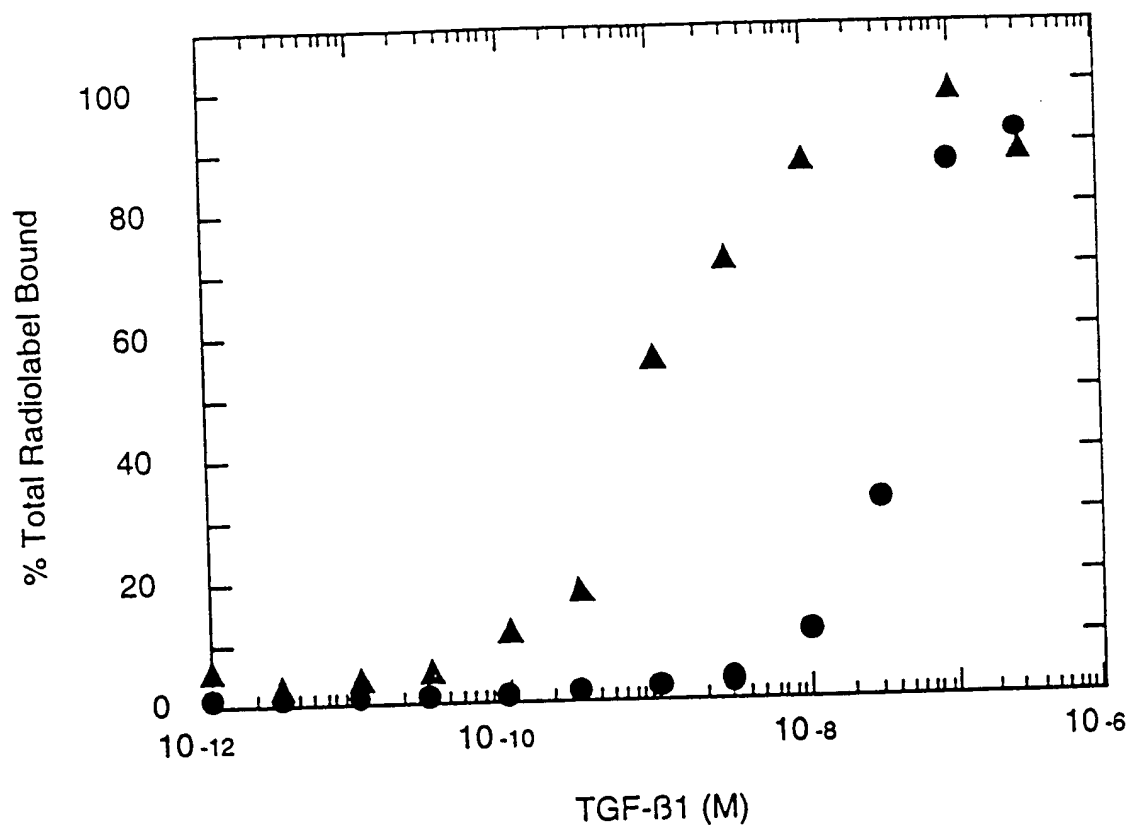


FIGURE 1

2/17

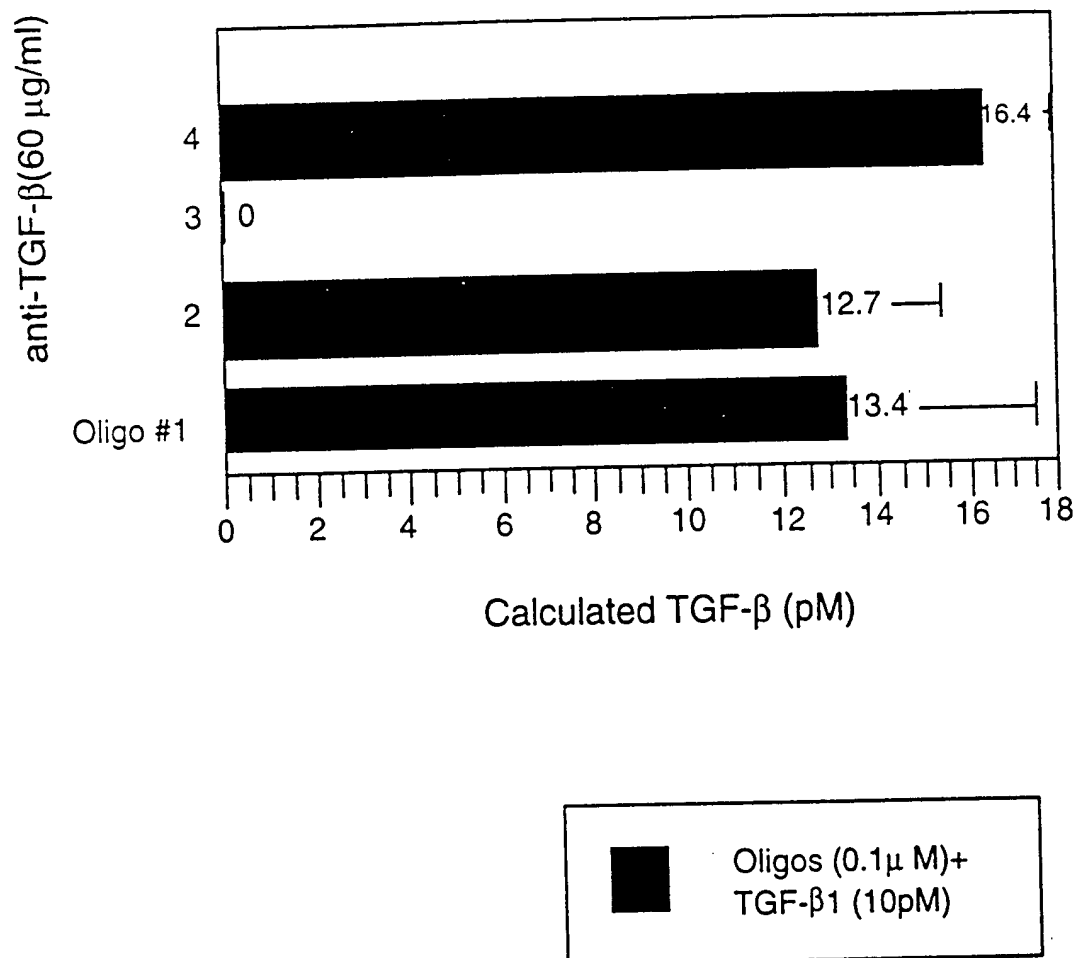
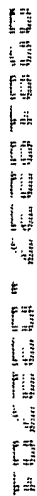


FIGURE 2

1



1

10

4/17

36t  
 C C G T A C T C A C  
 G G C A T A G T A  
 G C  
 G C  
 A T  
 C G  
 A T  
 5' C-G[3'T]

SEQ ID NO: 173

20t  
 C T T G T G T C T T  
 T T G C G T G A C T T  
 G C  
 G C  
 5' TGGGA G-C G[3'T]

SEQ ID NO: 172

41t  
 5' T A C T C A G C T G C A A A  
 [3'T] A T G A G T C G C A C T G T A  
 G C  
 G C  
 G C  
 T A

SEQ ID NO: 174

FIGURE 4

5/17

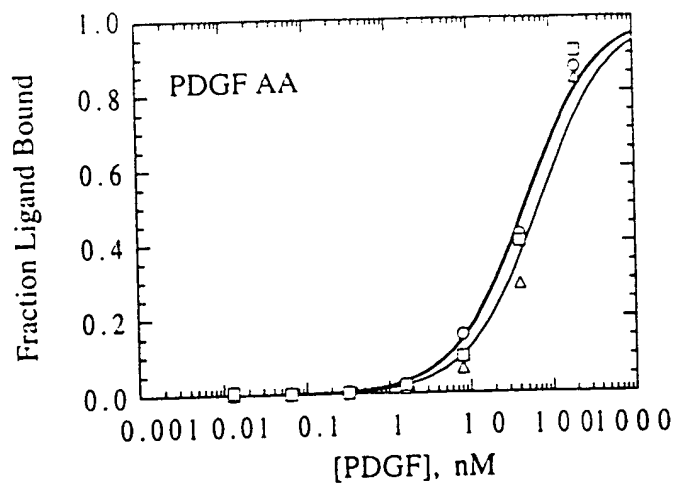


Figure 5A

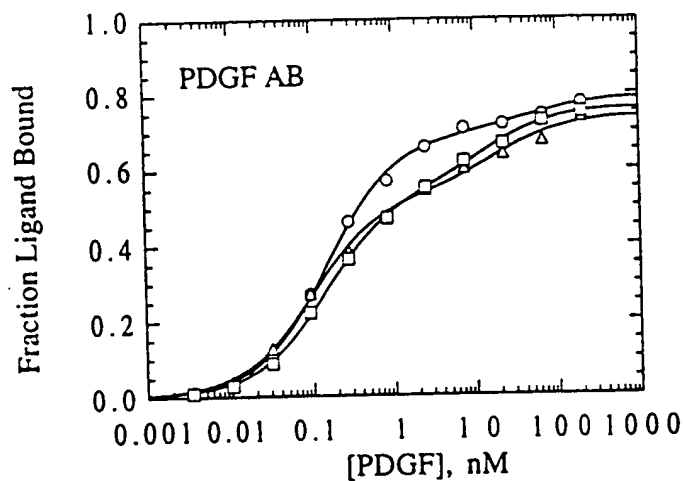


Figure 5B

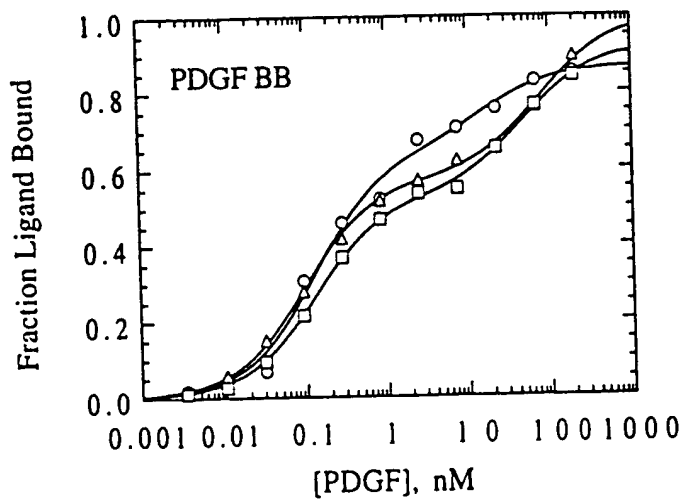


Figure 5C

SUBSTITUTE SHEET (RULE 26)

6/17

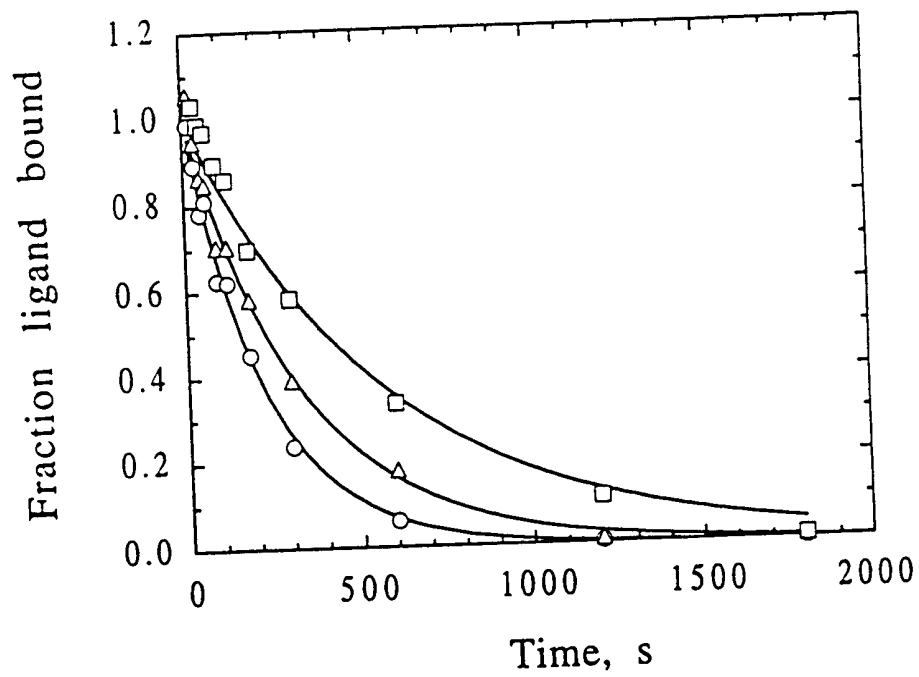


FIGURE 6

7/17

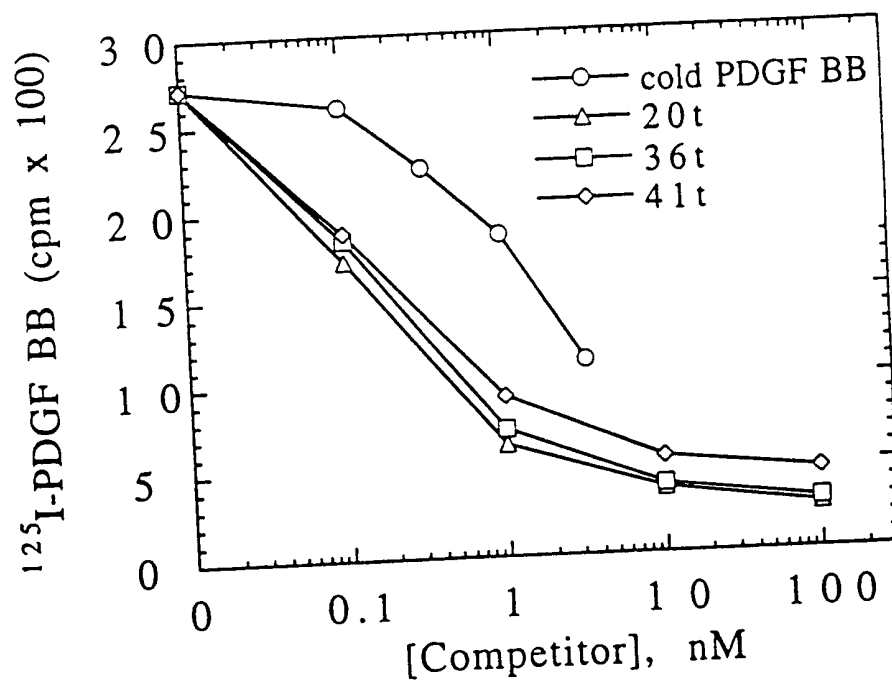


FIGURE 7

8/17

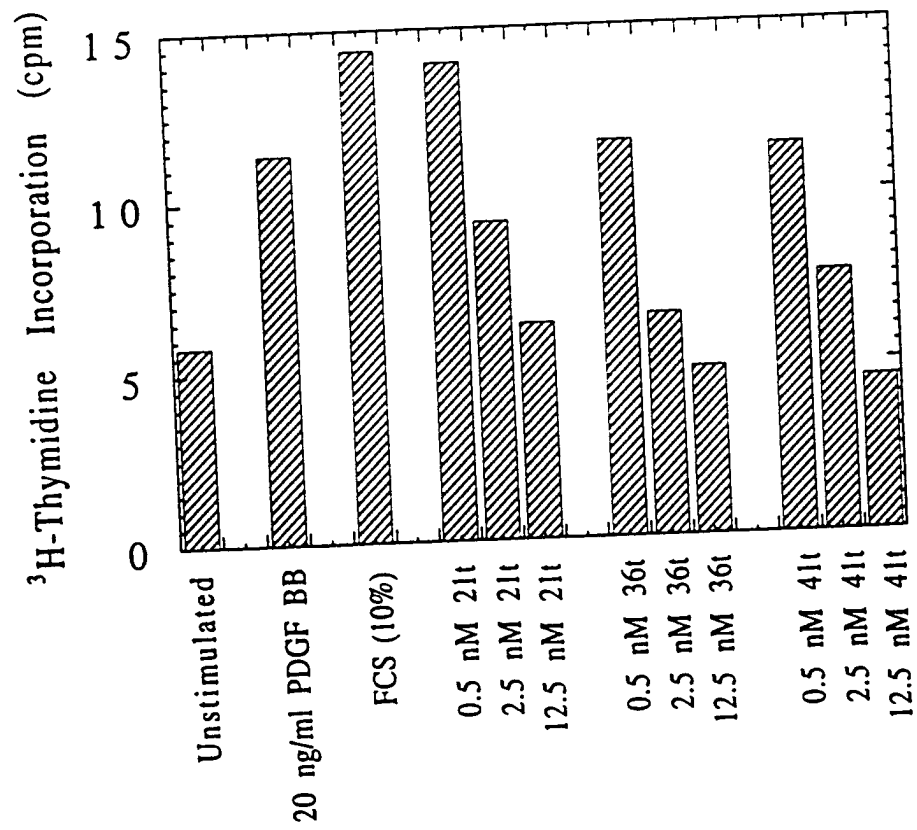
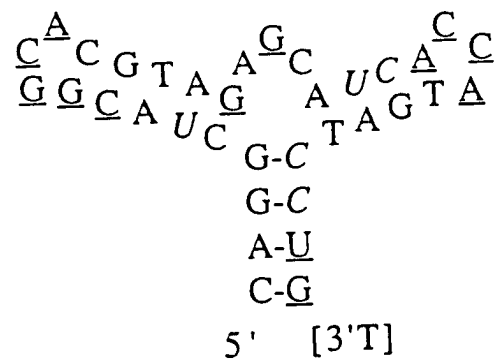


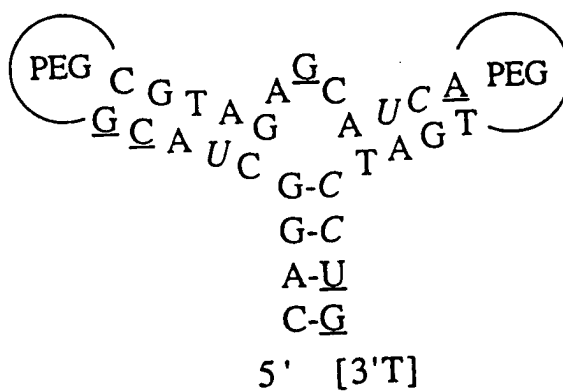
FIGURE 8



9/17

 $K_d=0.065$  nM

SEQ ID NO: 175

 $K_d=0.097$  nM

SEQ ID NO: 176

FIGURE 9

10/17

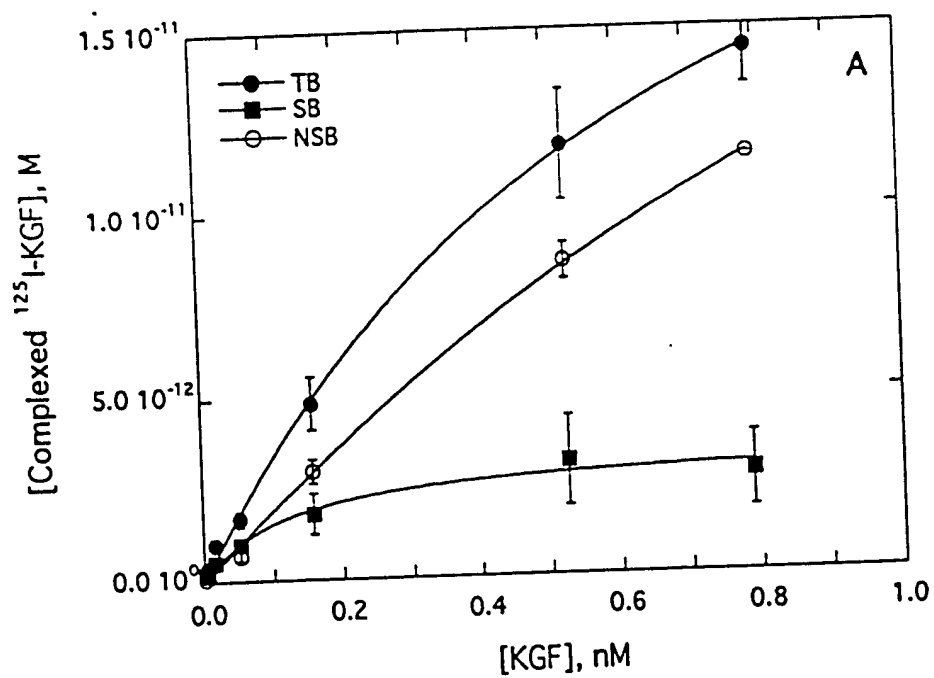


FIGURE 10A

11/17

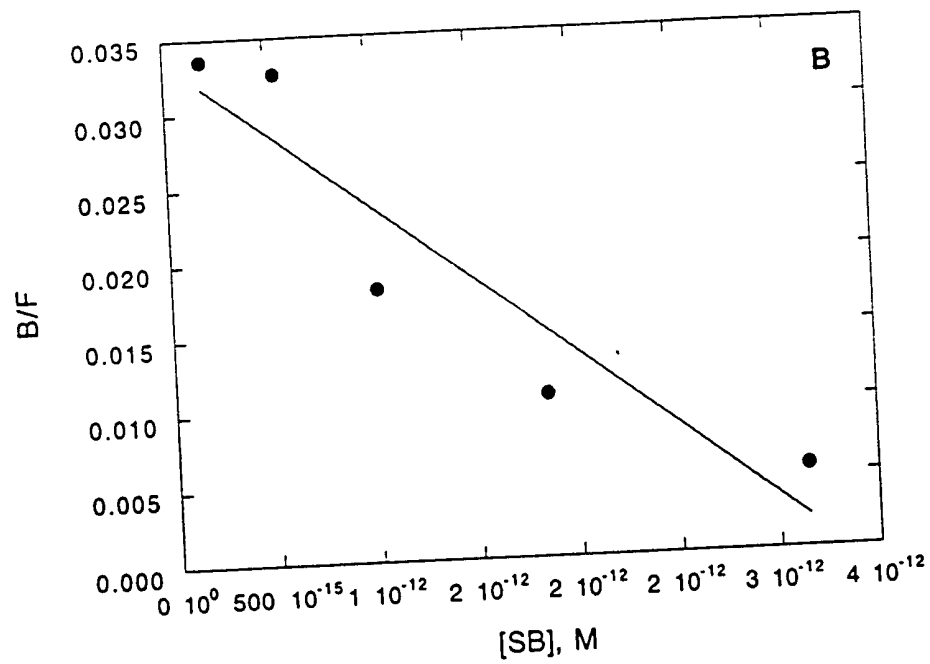


FIGURE 10B

12/17

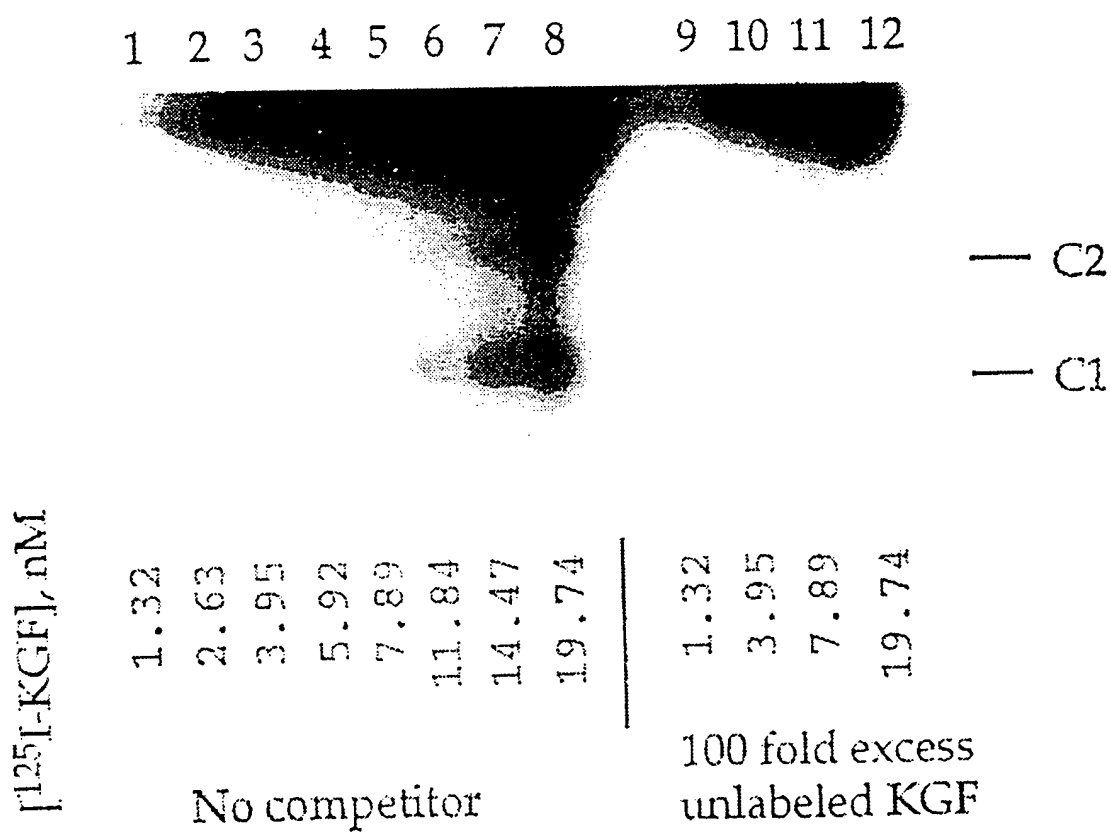


FIGURE 11

Class 1

SEQ ID NO:	Clone	Kd, nM	Ki, nM	
231	*14F	0.001	3.3	gaaaga
223	*6F	0.05	1.3	gaaagaa
232	*15F	0.07	6.7	gaaagaaaca
259	*56F	0.07	0.3	gaaagaaaca
240	*26F	0.23		AACAGUCUG
246	37F	0.46	6.7	acgaugacaa
233	*16F	0.83		gaaaga
249	42F	0.9		gaaaga
244	31F	1.0		gaaaggaacgaugcgaacgaug
245	35F	1.1		gaaaga
257	54F	1.23		gaaaga
255	51F	1.27		gaaaga
220	2F	1.77		gaaagaaacaa
239	24F	2.02		gaaaga
262	60F	2.1		gaaaga
238	23F	2.52		gaaagaa
222	5F	2.53		gaaagaaacgaugcgaacgaug
225	8F	2.63		gaaagaa
243	29F	3.24		gaaagaa
224	7F	3.69		gaaagaa
252	45F	4.7		gaaagaaacaa
268	Consensus			gGgagg

Summary Structure

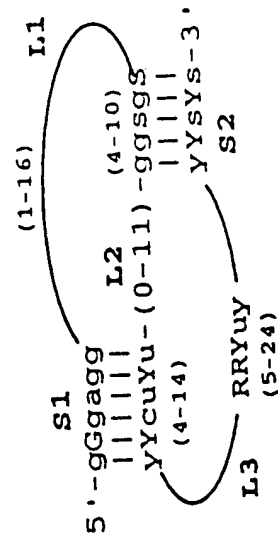
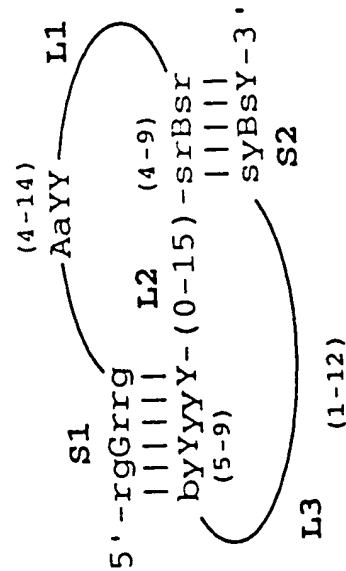


FIGURE 12A

## Class 2

[illegible]

## Summary Structure



**FIGURE 12B**

Class 1							
SEQ ID NO:	Clone	Kd, nM	KI, nM				
195	14N	0.4	2.0	UCCAGGGAU	UGAAGUGUGGGGUGAGGAACA	UAAAG	GCGGCca
199	25N	0.9		augcgga	GGGAUG	CAACUA	GCAGAUACCAGCUGGCCagacga
191	4N	0.7	23.3	augcgga	AAGAGG	UAAAGAUACCAGG	CCcagac
189	1N	0.5	16.7	ggaagg	ACCAUAAAG	CAACAA	GUGGUGGCCcaga
205	36N	8.27		gga	ggaugcgga	UAAAG	ACAAGUCGAACAAAG
203	34N	0.8		augcgga	AAGAGCU	CAGUC	ACAGUC
207	42N	0.8	266.7	augcgga	ACCU	CA CU	GCGGCCag
196	16N	1.4		cgauugcgga	AGUUCUACAAAGUUGGAA	Yaa	UGUacaga
	Consensus			GGG	aa	gA	CCC

Summary Structure

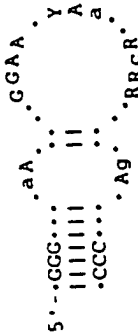


FIGURE 12C

Class 2	SEQ ID NO	Clone	K <sub>d</sub> , nM	K <sub>i</sub> , nM	AGGAAGGUCAGAGGAAA gacgaugcg AGAAGAUGCA ugcgggcuuag acgaugcaggc	GUUGGAAGA GGAACAGCGAAA GGAAA AGGAGCAA	CAGC UGAG UGUU UGAACUACUACAAGCCGUGCCACGU	CGUU CCGGUCG UGCGU CUGAG	CGGG IGCAGU GUGG GUGG CGGC	GUGcagacga AAUGUGAC Ccagacgac Ucagacgac agacgacuc	cucgcccga ACUGCGGca ucgcccga ucgcccga gcccga
209	47N	1.8								CGAA	GACC
198	24N	1.2									
202	29N	0.43		13.3							
204	35N	2.3		26.7							
192	6N	0.7									
190	2N	0.8		66.7							
211	54N	5.3									
271		Consensus									

# Summary Structure

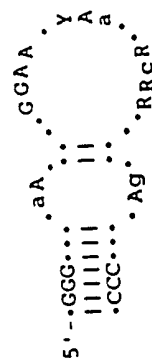
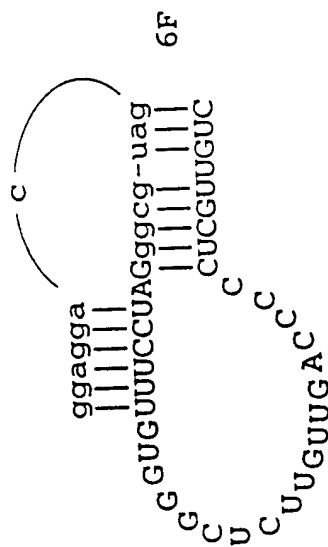


FIGURE 12D



6F gggaggacgagcggGAUCCUUUGUGGGCUUUGUGACCCCCUCCUUGUCCCCCccagacgacucgccccga

SEQ ID NO: 223



14F gggaggacgaugcggUGGUCUCCCAAUUCUAAA CUUUCUCCAUCCGUAUCUGGGCcagacgacucgccccga

SEQ ID NO: 231

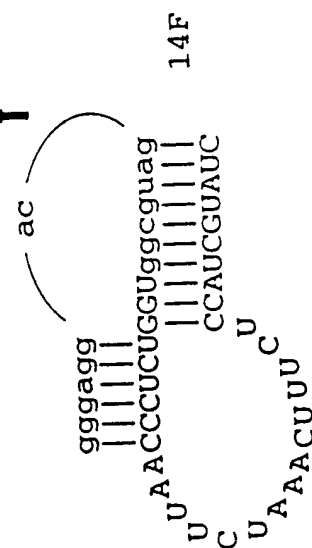


FIGURE 13